

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/423,194ADATE: 02/23/97
TIME: 07:42:39

INPUT SET: S15803.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

1
2
3 (1) General Information:
4
5 (i) APPLICANT: Eaton, Dan L.
6 de Sauvage, Frederic J.
7
8 (ii) TITLE OF INVENTION: MPL LIGAND
9
10 (iii) NUMBER OF SEQUENCES: 77
11
12 (iv) CORRESPONDENCE ADDRESS:
13 (A) ADDRESSEE: Genentech, Inc.
14 (B) STREET: 460 Point San Bruno Blvd
15 (C) CITY: South San Francisco
16 (D) STATE: California
17 (E) COUNTRY: USA
18 (F) ZIP: 94080
19
20 (v) COMPUTER READABLE FORM:
21 (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
22 (B) COMPUTER: IBM PC compatible
23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24 (D) SOFTWARE: WinPatin (Genentech)
25
26 (vi) CURRENT APPLICATION DATA:
27 (A) APPLICATION NUMBER: 08/423194
28 (B) FILING DATE: 18-Apr-1995
29 (C) CLASSIFICATION:
30
31 (vii) PRIOR APPLICATION DATA:
32 (A) APPLICATION NUMBER: 08/249376
33 (B) FILING DATE: 25-MAY-1994
34
35 (vii) PRIOR APPLICATION DATA:
36 (A) APPLICATION NUMBER: 08/223263
37 (B) FILING DATE: 04-APR-1994
38
39 (vii) PRIOR APPLICATION DATA:
40 (A) APPLICATION NUMBER: 08/196689
41 (B) FILING DATE: 15-FEB-1994
42
43 (vii) PRIOR APPLICATION DATA:
44 (A) APPLICATION NUMBER: 08/185607
45 (B) FILING DATE: 21-JAN-1994
46

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RAW SEQUENCE LISTING

PATENT APPLICATION US/08/423,194A

DATE: 02/28/97

TIME: 07:42:43

INPUT SET: S15803.raw

47 (vii) PRIOR APPLICATION DATA:
48 (A) APPLICATION NUMBER: 08/176553
49 (B) FILING DATE: 03-JAN-1994
50
51 (viii) ATTORNEY/AGENT INFORMATION:
52 (A) NAME: Winter, Daryl B.
53 (B) REGISTRATION NUMBER: 32,637
54 (C) REFERENCE/DOCKET NUMBER: P0871P4D2
55
56 (ix) TELECOMMUNICATION INFORMATION:
57 (A) TELEPHONE: 415/225-1249
58 (B) TELEFAX: 415/952-9881
59 (C) TELEX: 910/371-7168
60
61 (2) INFORMATION FOR SEQ ID NO:1:
62
63 (i) SEQUENCE CHARACTERISTICS:
64 (A) LENGTH: 353 amino acids
65 (B) TYPE: Amino Acid
66 (D) TOPOLOGY: Linear
67
68 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
69
70 Met Glu Leu Thr Glu Leu Leu Leu Val Val Met Leu Leu Leu Thr
71 -21 -20 -15 -10
72
73 Ala Arg Leu Thr Leu Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu
74 -5 1 5
75
76 Arg Val Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu His Ser
77 10 15 20
78
79 Arg Leu Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val
80 25 30 35
81
82 Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln
83 40 45 50
84
85 Met Glu Glu Thr Lys Ala Gln Asp Ile Leu Gly Ala Val Thr Leu
86 55 60 65
87
88 Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Gly Pro Thr
89 70 75 80
90
91 Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val Arg Leu
92 85 90 95
93
94 Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu Pro Pro
95 100 105 110
96
97 Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe Leu
98 115 120 125
99

RAW SEQUENCE LISTING PATENT APPLICATION US/98/423,194A

DATE: 02/28/97

TIME: 07:42:46

INPUT SET: S15803.raw

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100 Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met Leu
101 130 135 140
102
103 Val Gly Gly Ser Thr Leu Cys Val Arg Arg Ala Pro Pro Thr Thr
104 145 150 155
105
106 Ala Val Pro Ser Arg Thr Ser Leu Val Leu Thr Leu Asn Glu Leu
107 160 165 170
108
109 Pro Asn Arg Thr Ser Gly Leu Leu Glu Thr Asn Phe Thr Ala Ser
110 175 180 185
111
112 Ala Arg Thr Thr Gly Ser Gly Leu Leu Lys Trp Gln Gln Gly Phe
113 190 195 200
114
115 Arg Ala Lys Ile Pro Gly Leu Leu Asn Gln Thr Ser Arg Ser Leu
116 205 210 215
117
118 Asp Gln Ile Pro Gly Tyr Leu Asn Arg Ile His Glu Leu Leu Asn
119 220 225 230
120
121 Gly Thr Arg Gly Leu Phe Pro Gly Pro Ser Arg Arg Thr Leu Gly
122 235 240 245
123
124 Ala Pro Asp Ile Ser Ser Gly Thr Ser Asp Thr Gly Ser Leu Pro
125 250 255 260
126
127 Pro Asn Leu Gln Pro Gly Tyr Ser Pro Ser Pro Thr His Pro Pro
128 265 270 275
129
130 Thr Gly Gln Tyr Thr Leu Phe Pro Leu Pro Pro Thr Leu Pro Thr
131 280 285 290
132
133 Pro Val Val Gln Leu His Pro Leu Leu Pro Asp Pro Ser Ala Pro
134 295 300 305
135
136 Thr Pro Thr Pro Thr Ser Pro Leu Leu Asn Thr Ser Tyr Thr His
137 310 315 320
138
139 Ser Gln Asn Leu Ser Gln Glu Gly
140 325 330 332
141

```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1795 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/423,194A

DATE: 02/28/97

TIME: 07:42:50

INPUT SET: S15803.raw

153 TCTTCCTACC CATCTGCTCC CCAGAGGGCT GCCTGCTGTG CACTTGGGTC 50
154
155 CTGGAGCCCT TCTCCACCCG GATAGATTCC TCACCCCTTG CCCGCCTTTG 100
156
157 CCCCACCCCTA CTCTGCCCAG AAGTGCAAGA GCCTAAGCCG CCTCCATGGC 150
158
159 CCCAGGAAGG ATTCAGGGGA GAGGCCCCAA ACAGGGAGCC ACGCCAGCCA 200
160
161 GACACCCCGG CCAGAATGGA GCTGACTGAA TTGCTCCTCG TGGTCATGCT 250
162
163 TCTCCTAACT GCAAGGCTAA CGCTGTCCAG CCCGGCTCCT CCTGCTTGTG 300
164
165 ACCTCCGAGT CCTCAGTAAA CTGCTTCGTG ACTCCCATGT CCTTCACAGC 350
166
167 AGACTGAGCC AGTGCCCAGA GGTTCACCCCT TTGCCTACAC CTGTCTTGCT 400
168
169 GCCTGCTGTG GACTTTAGCT TGGGAGAATG GAAAACCCAG ATGGAGGAGA 450
170
171 CCAAGGCACA GGACATTCTG GGAGCAGTGA CCCTTCTGCT GGAGGGAGTG 500
172
173 ATGGCAGCAC GGGGACAACT GGGACCCACT TGCCTCTCAT CCCTCCTGGG 550
174
175 GCAGCTTTCT GGACAGGTCC GTCTCCTCCT TGGGGCCCTG CAGAGCCTCC 600
176
177 TTGGAACCCA GCTTCCTCCA CAGGGCAGGA CCACAGCTCA CAAGGATCCC 650
178
179 AATGCCATCT TCCTGAGCTT CCAACACCTG CTCCGAGGAA AGGTGCGTTT 700
180
181 CCTGATGCTT GTAGGAGGGT CCACCCCTG CGTCAGGCGG GCCCCACCCA 750
182
183 CCACAGCTGT CCCCAGCAGA ACCTCTCTAG TCCTCACACT GAACGAGCTC 800
184
185 CCAAACAGGA CTTCTGGATT GTTGGAGACA AACTTCACTG CCTCAGCCAG 850
186
187 AACTACTGGC TCTGGGCTTC TGAAGTGGCA GCAGGGATTC AGAGCCAAGA 900
188
189 TTCCTGGTCT GCTGAACCAA ACCTCCAGGT CCCTGGACCA AATCCCCGGA 950
190
191 TACCTGAACA GGATACACGA ACTCTTGAAT GGAACTCGTG GACTCTTTCC 1000
192
193 TGGACCCTCA CGCAGGACCC TAGGAGCCCC GGACATTTCC TCAGGAACAT 1050
194
195 CAGACACAGG CTCCCTGCCA CCAAACCTCC AGCCTGGATA TTCTCCTTCC 1100
196
197 CCAACCCATC CTCCTACTGG ACAGTATACG CTCTTCCCTC TTCCACCCAC 1150
198
199 CTTGCCCACC CCTGTGGTCC AGCTCCACCC CCTGCTTCCT GACCCTTCTG 1200
200
201 CTCCAACGCC CACCCCTACC AGCCCTCTTC TAAACACATC CTACACCCAC 1250
202
203 TCCCAGAATC TGTCTCAGGA AGGGTAAGGT TCTCAGACAC TGCCGACATC 1300
204
205 AGCATTGTCT CATGTACAGC TCCCTTCCCT GCAGGGCGCC CCTGGGAGAC 1350

INPUT SET: S15803.raw

206
207 AACTGGACAA GATTCCTAC TTTCTCCTGA AACCCAAAGC CCTGGTAAAA 1400
208
209 GGGATACACA GGAAGTAAAA GGAATCATT TTTCAGTGTG CATTATAAAC 1450
210
211 CTTCAGAAGC TATTTTTTTA AGCTATCAGC AATACTCATC AGAGCAGCTA 1500
212
213 GCTCTTTGGT CTATTTTCTG CAGAAATTTG CAACTCACTG ATTCTCTACA 1550
214
215 TGCTCTTTTT CTGTGATAAC TCTGCAAAGG CCTGGGCTGG CCTGGCAGTT 1600
216
217 GAACAGAGGG AGAGACTAAC CTTGAGTCAG AAAACAGAGA AAGGGTAATT 1650
218
219 TCCTTTGCTT CAAATTCAAG GCCTTCCAAC GCCCCATCC CCTTTACTAT 1700
220
221 CATCTCTAGT GGGACTCTGA TCCCATATTC TTAACAGATC TTTACTCTTG 1750
222
223 AGAAATGAAT AAGCTTTCTC TCAGAAAAAA AAAAAAAAAA AAAAA 1795
224

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

228 (A) LENGTH: 42 amino acids
229 (B) TYPE: Amino Acid
230 (D) TOPOLOGY: Linear
231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

232
233
234 Leu Leu Leu Val Val Met Leu Leu Leu Thr Ala Arg Leu Thr Leu
235 -16 -15 -10 -5
236
237 Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys
238 1 5 10
239
240 Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu
241 15 20 25 26
242

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

246 (A) LENGTH: 390 base pairs
247 (B) TYPE: Nucleic Acid
248 (C) STRANDEDNESS: Single
249 (D) TOPOLOGY: Linear
250

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

251
252
253
254 GAATTCCTGG AATACCAGCT GACAAATGATT TCCTCCTCAT CTTTCAACCT 50
255
256 CACCTCTCCT CATCTAAGAA TTGCTCCTCG TGGTCATGCT TCTCCTAACT 100
257
258 GCAAGGCTAA CGCTGTCCAG CCCGGCTCCT CCTGCTTGTG ACCTCCGAGT 150

PAGE: 1

SEQUENCE VERIFICATION REPORT

PATENT APPLICATION US/08/423,194A

DATE: 02/28/97

TIME: 07:42:57

INPUT SET: S15803.raw

Line	Error	Original Text
27	Wrong application Serial Number	(A) APPLICATION NUMBER: 08/423194